

05/90  
07/09

#6



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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/045,202

DATE: 07/11/2002

TIME: 16:11:19

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Output Set: N:\CRF3\07112002\J045202.raw

3 <110> APPLICANT: Bristol-Myers Squibb  
 4 Bristol-Myers Squibb  
 6 <120> TITLE OF INVENTION: MODULATORS OF BRUTON'S TYROSINE  
 KINASE  
 7 INTERMEDIATES AND METHODS FOR THEIR IDENTIFICATION AND USE IN THE TREATMENT AND  
 8 PREVENTION OF OSTEOPOROSIS AND RELATED DISEASE STATES  
 10 <130> FILE REFERENCE: D0032 NP  
 12 <140> CURRENT APPLICATION NUMBER: 10/045,202  
 C--> 13 <141> CURRENT FILING DATE: 2002-06-27  
 15 <150> PRIOR APPLICATION NUMBER: 60/242,471  
 16 <151> PRIOR FILING DATE: 2000-10-23  
 18 <160> NUMBER OF SEQ ID NOS: 12  
 20 <170> SOFTWARE: PatentIn version 3.1  
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 24 <212> TYPE: DNA  
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 48 cagacagccca aaaatgttat gggctccaa attttggaga acaggaatgg aagctaaaa 660  
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88	tccaaatttc	cagtccggtg	gtccccaccc	gaagtcctga	tgtatagcaa	gttcagcagc	1860											
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94	tacaggcctc	atctgcttc	agagaaggta	tataccatca	tgtacagttg	ttggcatgag	2040											
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135							50			55					60			
138	Glu	Thr	Val	Val	Pro	Glu	Lys	Asn	Pro	Pro	Pro	Glu	Arg	Gln	Ile	Pro		
139							65			70					75		80	
142	Arg	Arg	Gly	Glu	Glu	Ser	Ser	Glu	Met	Glu	Gln	Ile	Ser	Ile	Ile	Glu		
143								85			90					95		
146	Arg	Phe	Pro	Tyr	Pro	Phe	Gln	Val	Val	Tyr	Asp	Glu	Gly	Pro	Leu	Tyr		
147								100			105					110		
150	Val	Phe	Ser	Pro	Thr	Glu	Glu	Leu	Arg	Lys	Arg	Trp	Ile	His	Gln	Leu		
151								115			120					125		
154	Lys	Asn	Val	Ile	Arg	Tyr	Asn	Ser	Asp	Leu	Val	Gln	Lys	Tyr	His	Pro		
155								130			135					140		
158	Cys	Phe	Trp	Ile	Asp	Gly	Gln	Tyr	Leu	Cys	Cys	Ser	Gln	Thr	Ala	Lys		
159								145			150					155		160
162	Asn	Ala	Met	Gly	Cys	Gln	Ile	Leu	Glu	Asn	Arg	Asn	Gly	Ser	Leu	Lys		
163									165			170				175		
166	Pro	Gly	Ser	Ser	His	Arg	Lys	Thr	Lys	Lys	Pro	Leu	Pro	Pro	Thr	Pro		
167									180			185				190		
170	Glu	Glu	Asp	Gln	Ile	Leu	Lys	Lys	Pro	Leu	Pro	Pro	Glu	Pro	Ala	Ala		
171									195			200				205		
174	Ala	Pro	Val	Ser	Thr	Ser	Glu	Leu	Lys	Lys	Val	Val	Ala	Leu	Tyr	Asp		

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182	Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp		
183	245	250	255
186	Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala		
187	260	265	270
190	Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg		
191	275	280	285
194	Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe		
195	290	295	300
198	Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe		
199	305	310	315
			320
202	Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val		
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206	Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe		
207	340	345	350
210	Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly		
211	355	360	365
214	Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala		
215	370	375	380
218	Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys		
219	385	390	395
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222	Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val		
223	405	410	415
226	Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile		
227	420	425	430
230	Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val		
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234	Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys		
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238	Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly		
239	465	470	475
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242	Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln		
243	485	490	495
246	Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu		
247	500	505	510
250	Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu		
251	515	520	525
254	Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg		
255	530	535	540
258	Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro		
259	545	550	555
			560
262	Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser		
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266	Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser		
267	580	585	590
270	Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu		
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 278 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu  
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300 agagaggaag	ccatggctgc	agtatactg	gagagcatct	ttctgaagcg	ctcccagcag	180
302 aaaaagaaaa	catcacctt	aaacttcaag	aaggcctgt	ttctcttgac	tgtacacaaa	240
304 ctttcatact	atgaatatga	ctttaaacgt	gggagaagag	gcagtaagaa	aggttcaata	300
306 gatgttggaa	agatcacctg	tgttggaaaca	gtaattcctg	aaaaaaatcc	cccaccagaa	360
308 agacagatc	cgaggagagg	tgaggagatc	agtaaaatgg	aacagatttc	aatcattgaa	420
310 aggttcccg	accatttca	ggttgtat	gatgaaggac	ctctctatgt	tttctccca	480
312 actgaagagc	tgagaaagcg	ctggatttac	cagtcaaaaa	atgtaatccg	gtacaatagt	540
314 gacctggta	agaaatacca	tccttgctt	tggattgatg	gacagtatct	ctgctgtct	600
316 cagacagcca	agaatgtat	gggctgcca	atttggaga	acaggaatgg	aagcttaaaa	660
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356 tccaaatccc	cagtccggtg	gtctccacca	gaagtgccta	tgtatagcaa	gttcagcagc	1860
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360 ccgtatgaga	gatttactaa	cagtgagaca	gcagaacaca	ttgctcaagg	cttacgtctc	1980
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 397 35 40 45  
 400 Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val  
 401 50 55 60  
 404 Glu Thr Val Ile Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro  
 405 65 70 75 80  
 408 Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu  
 409 85 90 95  
 412 Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr  
 413 100 105 110  
 416 Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu  
 417 115 120 125  
 420 Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro  
 421 130 135 140  
 424 Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys  
 425 145 150 155 160  
 428 Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys  
 429 165 170 175  
 432 Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro  
 433 180 185 190  
 436 Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Thr Ala  
 437 195 200 205  
 440 Ala Pro Ile Ser Thr Thr Glu Leu Lys Lys Val Val Ala Leu Tyr Asp  
 441 210 215 220  
 444 Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Glu Glu  
 445 225 230 235 240  
 448 Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp  
 449 245 250 255  
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**VERIFICATION SUMMARY**

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